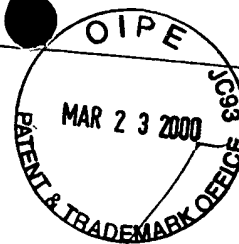


SEQUENCE LISTING



(1) GENERAL INFORMATION:

(i) APPLICANT: Beach, David H.
Demetrick, Douglas J.
Serrano, Manuel
Hannon, Gregory J.

(ii) TITLE OF INVENTION: Antibodies to Cell-Cycle Regulatory Proteins, and
Uses Related Thereto

(iii) NUMBER OF SEQUENCES: 34

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Foley, Hoag & Eliot
(B) STREET: One Post Office Square
(C) CITY: Boston
(D) STATE: MA
(E) COUNTRY: USA
(F) ZIP: 02109

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: WordPad

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: US 09/016,869
(B) FILING DATE: 30-JAN-1998

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/893,274
(B) FILING DATE: 15-JUL-1994

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/306,511
(B) FILING DATE: 14-SEP-1994

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/248,812
(B) FILING DATE: 25-MAY-1994

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/227,371
(B) FILING DATE: 14-APR-1994

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/154,915
(B) FILING DATE: 18-NOV-1993

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 07/991,997
(B) FILING DATE: 17-DEC-1992

(viii) ATTORNEY/AGENT INFORMATION:

- (A) NAME: Vincent, Matthew P.
- (B) REGISTRATION NUMBER: 36,709
- (C) REFERENCE/DOCKET NUMBER: MIV-071.10

(ix) TELECOMMUNICATION INFORMATION:

- (A) TELEPHONE: (617) 832-1299
- (B) TELEFAX: (617) 832-7000

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 994 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 41..508

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CGGAGAGGGG GAGAACAGAC AACGGGCGGC GGGGAGCAGC ATG GAT CCG GCG GCG	55
Met Asp Pro Ala Ala	
1 5	
GGG AGC AGC ATG GAG CCT TCG GCT GAC TGG CTG GCC ACG GCC GCG GCC	103
Gly Ser Ser Met Glu Pro Ser Ala Asp Trp Leu Ala Thr Ala Ala Ala	
10 15 20	
CGG GGT CGG GTA GAG GAG GTG CGG GCG CTG CTG GAG GCG GTG GCG CTG	151
Arg Gly Arg Val Glu Glu Val Arg Ala Leu Leu Glu Ala Val Ala Leu	
25 30 35	
CCC AAC GCA CCG AAT AGT TAC GGT CGG AGG CCG ATC CAG GTC ATG ATG	199
Pro Asn Ala Pro Asn Ser Tyr Gly Arg Arg Pro Ile Gln Val Met Met	
40 45 50	
ATG GGC AGC GCC CGA GTG GCG GAG CTG CTG CTG CTC CAC GGC GCG GAG	247
Met Gly Ser Ala Arg Val Ala Glu Leu Leu Leu Leu His Gly Ala Glu	
55 60 65	
CCC AAC TGC GCC GAC CCC GCC ACT CTC ACC CGA CCC GTG CAC GAC GCT	295
Pro Asn Cys Ala Asp Pro Ala Thr Leu Thr Arg Pro Val His Asp Ala	
70 75 80 85	
GCC CGG GAG GGC TTC CTG GAC ACG CTG GTG GTG CTG CAC CGG GCC GGG	343
Ala Arg Glu Gly Phe Leu Asp Thr Leu Val Val Leu His Arg Ala Gly	
90 95 100	
GCG CGG CTG GAC GTG CGC GAT GCC TGG GGC CGT CTG CCC GTG GAC CTG	391
Ala Arg Leu Asp Val Arg Asp Ala Trp Gly Arg Leu Pro Val Asp Leu	
105 110 115	
GCT GAG GAG CTG GGC CAT CGC GAT GTC GCA CGG TAC CTG CGC GCG GCT	439
Ala Glu Glu Leu Gly His Arg Asp Val Ala Arg Tyr Leu Arg Ala Ala	
120 125 130	
GCG GGG GGC ACC AGA GGC AGT AAC CAT GCC CGC ATA GAT GCC GCG GAA	487
Ala Gly Gly Thr Arg Gly Ser Asn His Ala Arg Ile Asp Ala Ala Glu	
135 140 145	
GGT CCC TCA GAC ATC CCC GAT TGAAAGAACC AGAGAGGCTC TGAGAAACCT	538
Gly Pro Ser Asp Ile Pro Asp	

(2) INFORMATION FOR SEQ ID NO:2:

(A) LENGTH: 156 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

91

(A) LENGTH: 837 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(A) NAME/KEY: CDS
(B) LOCATION: 328..738

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GAGGACTCCG CGACGGTCCG CACCCTGCGG CCAGAGCGGC TTTGAGCTCG GCTGCTTCCG 60
 CGCTAGGCGC TTTTTCCTCAG AAGCAATCCA GGCGCGCCCG CTGGTTCTTG AGCGCCAGGA 120
 AAAGCCCAGA GCTAACGACC GGCCGCTCGG CACTGCACGG GGCCCCAAGC CGCAGAAGAA 180
 GGACGACGGG AGGGTAATGA AGCTGAGCCC AGGTCTCCTA GGAAGGAGAG AGTCCGCCGG 240
 AGCAGCGTGG GAAAGAAGGG AAGAGTGTCG TTAAGTTTAC GGCCAACGGT GATTATCCG 300
 GGCCGCTGCG CGTCTGGGGG CTGCGGA ATG CGC GAG GAG AAC AAG GGC ATG 351

Met Arg Glu Glu Asn Lys Gly Met

1 5
 CCC AGT GGG GGC GGC AGC GAT GAG GGT CTG GCC ACG CCG GCG CGG GGA 399
 Pro Ser Gly Gly Gly Ser Asp Glu Gly Leu Ala Thr Pro Ala Arg Gly

10 15 20
 CTA GTG GAG AAG GTG CGA CAC TCC TGG GAA GCC GGC GCG GAT CCC AAC 447
 Leu Val Glu Lys Val Arg His Ser Trp Glu Ala Gly Ala Asp Pro Asn

25 30 35 40
 GGA GTC AAC CGT TTC GGG AGG CGC GCG ATC CAG GTC ATG ATG ATG GGC 495
 Gly Val Asn Arg Phe Gly Arg Arg Ala Ile Gln Val Met Met Met Gly

45 50 55
 AGC GCC CGC GTG GCG GAG CTG CTG CTG CTC CAC GGC GCG GAG CCC AAC 543
 Ser Ala Arg Val Ala Glu Leu Leu Leu Leu His Gly Ala Glu Pro Asn

60 65 70
 TGC GCA GAC CCT GCC ACT CTC ACC CGA CCG GTG CAT GAT GCT GCC CGG 591
 Cys Ala Asp Pro Ala Thr Leu Thr Arg Pro Val His Asp Ala Ala Arg

75 80 85
 GAG GGC TTC CTG GAC ACG CTG GTG GTG CTG CAC CGG GCC GGG GCG CGG 639
 Glu Gly Phe Leu Asp Thr Leu Val Val Leu His Arg Ala Gly Ala Arg

90 95 100
 CTG GAC GTG CGC GAT GCC TGG GGT CGT CTG CCC GTG GAC TTG GCC GAG 687
 Leu Asp Val Arg Asp Ala Trp Gly Arg Leu Pro Val Asp Leu Ala Glu

105 110 115 120
 GAG CGG GGC CAC CGC GAC GTT GCA GGG TAC CTG CGC ACA GCC ACG GGG 735
 Glu Arg Gly His Arg Asp Val Ala Gly Tyr Leu Arg Thr Ala Thr Gly

125 130 135
 GAC TGACGCCAGG TTCCCCAGCC GCCCACAACG ACTTTATTTT CTTACCCAAT 788
 Asp

TTCCACCCCC CACCCACCTA ATTCGATGAA GGCTGCCAAC GGGGAGCGG 837

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 137 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Arg Glu Glu Asn Lys Gly Met Pro Ser Gly Gly Gly Ser Asp Glu
 1 5 10 15
 Gly Leu Ala Thr Pro Ala Arg Gly Leu Val Glu Lys Val Arg His Ser
 20 25 30
 Trp Glu Ala Gly Ala Asp Pro Asn Gly Val Asn Arg Phe Gly Arg Arg
 35 40 45
 Ala Ile Gln Val Met Met Met Gly Ser Ala Arg Val Ala Glu Leu Leu
 50 55 60
 Leu Leu His Gly Ala Glu Pro Asn Cys Ala Asp Pro Ala Thr Leu Thr

65 70 75 80
 Arg Pro Val His Asp Ala Ala Arg Glu Gly Phe Leu Asp Thr Leu Val
 85 90 95
 Val Leu His Arg Ala Gly Ala Arg Leu Asp Val Arg Asp Ala Trp Gly
 100 105 110
 Arg Leu Pro Val Asp Leu Ala Glu Glu Arg Gly His Arg Asp Val Ala
 115 120 125
 Gly Tyr Leu Arg Thr Ala Thr Gly Asp
 130 135

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 853 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: both
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
 (B) LOCATION: 213..587

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GGAGTACAGC AGCGGGAGCA TGGGTCGCAG GTTCTTGGTC ACTGTAAGGA TTCAGCGCGC 60
 GGGCCGCCCA CTCCAAGAGA GGGTTTCTCT GGTGAAGTTC GTGCGATCCC GGAGACCCAG 120
 GACAGCGAGC TCGCTCTGG CTTTCGTGAA CATGTTGTTG AGGCTAGAGA GGATCTTGAG 180
 AAGAGGGCCG CACCGGAATC CTGACCAGG TG ATG ATG ATG GGC AAC GTT CAC 233
 Met Met Met Gly Asn Val His
 1 5
 GTA GCA GCT CTT CTG CTC AAC TAC GGT GCA GAT TCG AAC TGC GAG GAC 281
 Val Ala Ala Leu Leu Leu Asn Tyr Gly Ala Asp Ser Asn Cys Glu Asp
 10 15 20
 CCC ACT ACC TTC TCC CGC CCG GTG CAC GAC GCA GCG CGG GAA GGC TTC 329
 Pro Thr Thr Phe Ser Arg Pro Val His Asp Ala Ala Arg Glu Gly Phe
 25 30 35
 CTG GAC ACG CTG GTG GTG CTG CAC GGG TCA GGG GCT CGG CTG GAT GTG 377
 Leu Asp Thr Leu Val Val Leu His Gly Ser Gly Ala Arg Leu Asp Val
 40 45 50 55
 CGC GAT GCC TGG GGT CGC CTG CCG CTC GAC TTG GCC CAA GAG CGG GGA 425
 Arg Asp Ala Trp Gly Arg Leu Pro Leu Asp Leu Ala Gln Glu Arg Gly
 60 65 70
 CAT CAA GAC ATC GTG CGA TAT TTG CGT TCC GCT GGG TGC TCT TTG TGT 473
 His Gln Asp Ile Val Arg Tyr Leu Arg Ser Ala Gly Cys Ser Leu Cys
 75 80 85
 TCC GCT GGG TGG TCT TTG TGT ACC GCT GGG AAC GTC GCC CAG ACC GAC 521

Ser Ala Gly Trp Ser Leu Cys Thr Ala Gly Asn Val Ala Gln Thr Asp
 90 95 100

GGG CAT AGC TTC AGC TCA AGC ACG CCC AGG GCC CTG GAA CTT CGC GGC 569
 Gly His Ser Phe Ser Ser Ser Thr Pro Arg Ala Leu Glu Leu Arg Gly
 105 110 115

CAA TCC CAA GAG CAG AGC TAAATCCGCC TCAGCCCGCC TTTTCTTCT 617
 Gln Ser Gln Glu Gln Ser
 120 125

TAGCTTCACT TCTAGCGATG CTAGCGTGTC TAGCATGTGG CTTTAAAAAA TACATAATAA 677

TGCTTTTTTTT GCAATCACGG GAGGGAGCAG AGGGAGGGAG CAGAAGGAGG GAGGGAGGGA 737

GGGAGGGACC TGGACAGGAA AGGAATGGCA TGAGAAACTG AGCGAAGGCG GCCGCGAAGG 797

GAATAATGGC TGGATTGTTT AAAAAAATAA AATAAAGATA CTTTTTAAAA TGTCAA 853

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 125 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met Met Met Gly Asn Val His Val Ala Ala Leu Leu Leu Asn Tyr Gly
 1 5 10 15

Ala Asp Ser Asn Cys Glu Asp Pro Thr Thr Phe Ser Arg Pro Val His
 20 25 30

Asp Ala Ala Arg Glu Gly Phe Leu Asp Thr Leu Val Val Leu His Gly
 35 40 45

Ser Gly Ala Arg Leu Asp Val Arg Asp Ala Trp Gly Arg Leu Pro Leu
 50 55 60

Asp Leu Ala Gln Glu Arg Gly His Gln Asp Ile Val Arg Tyr Leu Arg
 65 70 75 80

Ser Ala Gly Cys Ser Leu Cys Ser Ala Gly Trp Ser Leu Cys Thr Ala
 85 90 95

Gly Asn Val Ala Gln Thr Asp Gly His Ser Phe Ser Ser Ser Thr Pro
 100 105 110

Arg Ala Leu Glu Leu Arg Gly Gln Ser Gln Glu Gln Ser
 115 120 125

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 231 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: both
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 1..231

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GCA CTC CTG GAA GCC GGC GCA GAT CCC AAC GCC CTG AAC CGC TTC GGG 48
 Ala Leu Leu Glu Ala Gly Ala Asp Pro Asn Ala Leu Asn Arg Phe Gly
 1 5 10 15
 AGG CGC CCA ATC CAG GTC ATG ATG ATG GGC AGC GCC AGG GTG GCA GAG 96
 Arg Arg Pro Ile Gln Val Met Met Met Gly Ser Ala Arg Val Ala Glu
 20 25 30
 CTG CTG CTG CTC CAC GGA GCA GAA CCC AAC TGC GCC GAC CCT GCC ACC 144
 Leu Leu Leu Leu His Gly Ala Glu Pro Asn Cys Ala Asp Pro Ala Thr
 35 40 45
 CTT ACC AGA CCT GTG CAC GAC GCA GCT CGG GAA GGC TTC CTG GAC ACG 192
 Leu Thr Arg Pro Val His Asp Ala Ala Arg Glu Gly Phe Leu Asp Thr
 50 55 60
 CTT GTC GTG CTG CAC CGG GCA GGG GCG CGG TTG GAT GTG 231
 Leu Val Val Leu His Arg Ala Gly Ala Arg Leu Asp Val
 65 70 75

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 77 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Ala Leu Leu Glu Ala Gly Ala Asp Pro Asn Ala Leu Asn Arg Phe Gly
 1 5 10 15
 Arg Arg Pro Ile Gln Val Met Met Met Gly Ser Ala Arg Val Ala Glu
 20 25 30
 Leu Leu Leu Leu His Gly Ala Glu Pro Asn Cys Ala Asp Pro Ala Thr
 35 40 45
 Leu Thr Arg Pro Val His Asp Ala Ala Arg Glu Gly Phe Leu Asp Thr
 50 55 60
 Leu Val Val Leu His Arg Ala Gly Ala Arg Leu Asp Val
 65 70 75

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 303 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: N-terminal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Met Ala Thr Ser Arg Tyr Glu Pro Val Ala Glu Ile Gly Val Gly Ala
1 5 10 15
Tyr Gly Thr Val Tyr Lys Ala Xaa Asp Pro His Ser Gly His Phe Val
20 25 30
Ala Leu Lys Ser Val Arg Val Pro Asn Gly Gly Gly Gly Gly Gly Gly
35 40 45
Leu Pro Ile Ser Thr Val Arg Glu Val Ala Leu Leu Arg Arg Leu Glu
50 55 60
Ala Phe Glu His Pro Asn Val Val Arg Leu Met Asp Val Cys Ala Thr
65 70 75 80
Ser Arg Thr Asp Arg Glu Ile Lys Val Thr Leu Val Phe Glu His Val
85 90 95
Asp Gln Asp Leu Arg Thr Tyr Leu Asp Lys Ala Pro Pro Pro Gly Leu
100 105 110
Pro Ala Glu Thr Ile Lys Asp Leu Met Arg Gln Phe Leu Arg Gly Leu
115 120 125
Asp Phe Leu His Ala Asn Cys Ile Val His Arg Asp Leu Lys Pro Glu
130 135 140
Asn Ile Leu Val Thr Ser Gly Gly Thr Val Lys Leu Ala Asp Phe Gly
145 150 155 160
Leu Ala Arg Ile Tyr Ser Tyr Gln Met Ala Leu Thr Pro Val Val Val
165 170 175
Thr Leu Trp Tyr Arg Ala Pro Glu Val Leu Leu Gln Ser Thr Tyr Ala
180 185 190
Thr Pro Val Asp Met Trp Ser Val Gly Cys Ile Phe Ala Glu Met Phe
195 200 205
Arg Arg Lys Pro Leu Phe Cys Gly Asn Ser Glu Ala Asp Gln Leu Gly
210 215 220
Lys Ile Phe Asp Leu Ile Gly Leu Pro Pro Glu Asp Asp Trp Pro Arg
225 230 235 240

Asp Val Ser Leu Pro Arg Gly Ala Phe Pro Pro Arg Gly Pro Arg Pro
 245 250 255
 Val Gln Ser Val Val Pro Glu Met Glu Glu Ser Gly Ala Gln Leu Leu
 260 265 270
 Leu Glu Met Leu Thr Phe Asn Pro His Lys Arg Ile Ser Ala Phe Arg
 275 280 285
 Ala Leu Gln His Ser Tyr Leu His Lys Asp Glu Gly Asn Pro Glu
 290 295 300

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 326 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: N-terminal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Met Glu Lys Asp Gly Leu Cys Arg Ala Asp Gln Gln Tyr Glu Cys Val
 1 5 10 15
 Ala Glu Ile Gly Glu Gly Ala Tyr Gly Lys Val Phe Lys Ala Xaa Asp
 20 25 30
 Leu Lys Asn Gly Gly Arg Phe Val Ala Leu Lys Arg Val Arg Val Gln
 35 40 45
 Thr Gly Glu Glu Gly Met Pro Leu Ser Thr Ile Arg Glu Val Ala Val
 50 55 60
 Leu Arg His Leu Glu Thr Phe Glu His Pro Asn Val Val Arg Leu Phe
 65 70 75 80
 Asp Val Cys Thr Val Ser Arg Thr Asp Arg Glu Thr Lys Leu Thr Leu
 85 90 95
 Val Phe Glu His Val Asp Gln Asp Leu Thr Thr Tyr Leu Asp Lys Val
 100 105 110
 Pro Glu Pro Gly Val Pro Thr Glu Thr Ile Lys Asp Met Met Phe Gln
 115 120 125
 Leu Leu Arg Gly Leu Asp Phe Leu His Ser His Arg Val Val His Arg
 130 135 140
 Asp Leu Lys Pro Gln Asn Ile Leu Val Thr Ser Ser Gly Gln Ile Lys
 145 150 155 160

Leu Ala Asp Phe Gly Leu Ala Arg Ile Tyr Ser Phe Gln Met Ala Leu
 165 170 175

Thr Ser Val Val Val Thr Leu Trp Tyr Arg Ala Pro Glu Val Leu Leu
 180 185 190

Gln Ser Ser Tyr Ala Thr Pro Val Asp Leu Trp Ser Val Gly Cys Ile
 195 200 205

Phe Ala Glu Met Phe Arg Arg Lys Pro Leu Phe Arg Gly Ser Ser Asp
 210 215 220

Val Asp Gln Leu Gly Lys Ile Leu Asp Val Ile Gly Leu Pro Gly Glu
 225 230 235 240

Glu Asp Trp Pro Arg Asp Val Ala Leu Pro Arg Gln Ala Phe His Ser
 245 250 255

Lys Ser Ala Gln Pro Ile Glu Lys Phe Val Thr Asp Ile Asp Glu Leu
 260 265 270

Gly Lys Asp Leu Leu Leu Lys Cys Leu Thr Phe Asn Pro Ala Lys Arg
 275 280 285

Ile Ser Ala Tyr Ser Ala Leu Ser His Pro Tyr Phe Gln Asp Leu Glu
 290 295 300

Arg Cys Lys Glu Asn Leu Asp Ser His Leu Pro Pro Ser Gln Asn Thr
 305 310 315 320

Ser Glu Leu Asn Thr Ala
 325

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 85 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Met Met Met Gly Xaa Xaa Xaa Val Ala Xaa Leu Leu Leu Xaa Xaa Gly
 1 5 10 15

Ala Xaa Xaa Asn Cys Xaa Asp Pro Xaa Thr Xaa Xaa Xaa Arg Pro Val
 20 25 30

His Asp Ala Ala Arg Glu Gly Phe Leu Asp Thr Leu Val Val Leu His
 35 40 45
 Xaa Xaa Gly Ala Arg Leu Asp Val Arg Asp Ala Trp Gly Arg Leu Pro
 50 55 60
 Xaa Asp Leu Ala Xaa Glu Xaa Gly His Xaa Asp Xaa Xaa Xaa Tyr Leu
 65 70 75 80
 Arg Xaa Ala Xaa Gly
 85

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 157 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Met Asp Pro Ala Ala Gly Ser Ser Met Glu Pro Ser Ala Asp Trp Leu
 1 5 10 15
 Ala Thr Ala Ala Ala Arg Gly Arg Val Glu Glu Val Arg Ala Leu Leu
 20 25 30
 Glu Ala Val Ala Leu Pro Asn Ala Pro Asn Ser Tyr Gly Arg Arg Pro
 35 40 45
 Ile Gln Val Met Met Met Gly Xaa Xaa Xaa Val Ala Xaa Leu Leu Leu
 50 55 60
 Xaa Xaa Gly Ala Xaa Xaa Asn Cys Xaa Asp Pro Xaa Thr Xaa Xaa Xaa
 65 70 75 80
 Arg Pro Val His Asp Ala Ala Arg Glu Gly Phe Leu Asp Thr Leu Val
 85 90 95
 Val Leu His Xaa Xaa Gly Ala Arg Leu Asp Val Arg Asp Ala Trp Gly
 100 105 110
 Arg Leu Pro Xaa Asp Leu Ala Xaa Glu Xaa Gly His Xaa Asp Xaa Xaa
 115 120 125
 Xaa Tyr Leu Arg Xaa Ala Xaa Gly Gly Thr Arg Gly Ser Asn His Ala
 130 135 140
 Arg Ile Asp Ala Ala Glu Gly Pro Ser Asp Ile Pro Asp

145

150

155

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 138 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Met Arg Glu Glu Asn Lys Gly Met Pro Ser Gly Gly Gly Ser Asp Glu
1 5 10 15

Gly Leu Ala Thr Pro Ala Arg Gly Leu Val Glu Lys Val Arg His Ser
20 25 30

Trp Glu Ala Gly Ala Asp Pro Asn Gly Val Asn Arg Phe Gly Arg Arg
35 40 45

Ala Ile Gln Val Met Met Met Gly Xaa Xaa Xaa Val Ala Xaa Leu Leu
50 55 60

Leu Xaa Xaa Gly Ala Xaa Xaa Asn Cys Xaa Asp Pro Xaa Thr Xaa Xaa
65 70 75 80

Xaa Arg Pro Val His Asp Ala Ala Arg Glu Gly Phe Leu Asp Thr Leu
85 90 95

Val Val Leu His Xaa Xaa Gly Ala Arg Leu Asp Val Arg Asp Ala Trp
100 105 110

Gly Arg Leu Pro Xaa Asp Leu Ala Xaa Glu Xaa Gly His Xaa Asp Xaa
115 120 125

Xaa Xaa Tyr Leu Arg Xaa Ala Xaa Gly Asp
130 135

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 127 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Met Met Met Gly Xaa Xaa Xaa Val Ala Xaa Leu Leu Leu Xaa Xaa Gly
1 5 10 15
Ala Xaa Xaa Asn Cys Xaa Asp Pro Xaa Thr Xaa Xaa Xaa Arg Pro Val
20 25 30
His Asp Ala Ala Arg Glu Gly Phe Leu Asp Thr Leu Val Val Leu His
35 40 45
Xaa Xaa Gly Ala Arg Leu Asp Val Arg Asp Ala Trp Gly Arg Leu Pro
50 55 60
Xaa Asp Leu Ala Xaa Glu Xaa Gly His Xaa Asp Xaa Xaa Xaa Tyr Leu
65 70 75 80
Arg Xaa Ala Xaa Gly Cys Ser Leu Cys Ser Ala Gly Trp Ser Leu Cys
85 90 95
Thr Ala Gly Asn Val Ala Gln Thr Asp Gly His Ser Phe Ser Ser Ser
100 105 110
Thr Pro Arg Ala Leu Glu Leu Arg Gly Gln Ser Gln Glu Gln Ser
115 120 125

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Val Ala Glu Ile Gly Xaa Gly Ala Tyr Gly Xaa Val Xaa Lys Ala Arg Asp
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids

- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Val Xaa Lys Ala Arg Asp
1 5

(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 4 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Lys Ala Arg Asp
1

(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 960 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

CGGAGAGGGA ATTCGACACGA GGCAGCATG GAGCCTTCGG CTGACTGGCT GGCCACGGCC	60
GCGGCCCCGGG GTCCGGTAGA GGAGGTGCGG GCGCTGCTGG AGGCGGTGGC GCTGCCCCAA	120
CGCACCGAAT AGTTACGGTC GGAGGCCGAT CCAGGTCATG GATGATGGGC AGCGCCCCGA	180
GTGGCGGAGC TCTGCTGCT CCACGGCGCG GAGCCCAACT GCGCCGACCC CGCCACTCTC	240
ACCCGACCCG TGCACCACGC TGCCCGGGAG GGCTTCTGGA CACGCTGGTG GTGCTGCACC	300
GGGCCGGGGC GCGGCTGGAC GTGCGCGATG CCTGGGGCCG TCTGCCCCGTG GACCTGGCTG	360
AGGAGCTGGG CCATCGCGAT GTCGCACGGT ACCTGCGCGC CCGTGCGGGG GGCACCAGAG	420

GCAGTAACCA TGCCCGCATA GATGCCGCGG AAGGTCCCTC AGACATCCCC GATTGAAAGA 480
ACCAGAGAGG CTCTGAGAAA CCTCGGGAAA CTTAGATCAT CAGTCACCGA AGGTCCTACA 540
GGGCCACAAC TGCCCCCGCC ACAACCCACC CCGCTTTCGT AGTTTTTCATT TAGAAAAATAG 600
AGCTTTTAAA AATGTCCTGC CTTTAAACGT AGATATAAGC CTTCCCCCAC TACCGTAAAT 660
GTCCATTTAT ATCATTTTTT ATATATTCTT ATAAAAATGT AAAAAAAGAA AAACACCGCT 720
TCTGCCTTTT CACTGTGTTG GAGTTTCTG GAGTGAGCAC TCACGCCCTA AGCGCACATT 780
CATGTGGGCA TTTCTTGCGA GCCTCGCAGC CTCCGGAAGC TGTGCACTTC ATGACAAGCA 840
TTTTGTGAAC TAGGGAAGCT CAGGGGGGTT ACTGGCTTCT CTTGAGTCAC ACTGCTAGCA 900
AATGGCAGAA CCAAAGCTCA AATAAAAATA AAATTATTTT CATTCAATCA CTCAAAAAAA 960

(2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 334 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

GGNGGNAAGN TGTGGGGGAA AGTTTGGGGA TGGAANACCA ANCCCTCCTT TCNTTACCAA 60
ACNCTGGCTC TGNCGAGGCT NCNTCCGANT GGTNCCCCCG GGGGAGACCC AACCTGGGNC 120
GACTTCAGGG NTGCNACATT CATTCATAA GTGCTNGGAG NTAATANCAC CTCCTCCGAG 180
CANNGACAGG NTCGAGGGG GCTCTTCCCC CANCACCGGA GGAAGAAAGA GGAGGGNCTN 240
CGGAGAGGGG GAGAACAGAC AACGGGCGGC GGGGAGCAGC ATGGATCCGG CGGCGGGGAG 300
CAGCATGGAN CCTTCGACTG ACTGACTGCC TCGC 334

(2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 368 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

TCNCTTATTG NTAGGANATA ATAACACCTC CACCGATAAC TTCACCTACA ACGTCCCNTT 60
TCCTGGAAAG ATACACAGCG TTCCCTCCAG AGGATTGTGT GGACAGGGTN GGAGNGGTCT 120
CTTCCNCCAC CACCGGAGGA AGAAAGAGGA GGGGCTGNCT GTTCACGAGA GGGTGGGACG 180
GACCNCGTAC GCTCGNCGNC TNCGGAGAGG GGGAGAGCAT CANCGGNCGN CGGGGAGCAA 240
CATGGAACCG NCGGCGGGGA GCAGCATGGA NCCTTCGGCT GACTGGCTGN CCACGNCCAC 300
GNCCCGGGGT CGGGTAGAGG AGGTGCGGNC GCTNCTGGAG GCGGGGNCTC TGNCCAACNC 360
GCTAAAN 368

(2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 404 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

GACNNCTCC GGCCGGNGTC GGGTAGAGGA GGTGCGGGCG CTGCTGGAGG CGGGGGCGCT 60
GCCCAACGCA CCGAATAGTT ACGGTCGGAG GCCGATCCAG GTNNGGGTAG AGGGTCTGCA 120
GCGGGAGCAG GGGATGGCGG GCGACTCTGG AGGACGAAGT TTGCAGGGGA ATTGGAATCA 180
GGTAGCGCTT CGATTCTCCN GAAAAAGGGG AGGCTTCCTG GGGAGTTTTT AGAAGGGGTT 240
TGTAATCACA GACCTCCTCC TGGCGACGTC CTGGGGGCTT GGAAGCCAA GGAAGAGGAA 300
TNAGGAGCCA CGCGGTACG AGTCTCTCGA ATGCTGAGAA GATCTNAAGG GGGGAACATA 360
TTTGTATTAG CNTCCAAGTN TNCTCTNTAT CANATACAAA NTNC 404

(2) INFORMATION FOR SEQ ID NO:22:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 401 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

CTCTNANCCC GGGTAGAGGG TCTGCAGCGG GAGCAGNGGA TGGCGGGCGA CTCTGGAGGA 60
CGAAGTTGGC AGGGGAATTG GAATCAGGTA GCGCTTCGAN TCTCCGAAA AAGGGGAGGC 120
TTCCTGGGGA GTTNNCAGAA GGGGTTTGTA ATCACAGNCC TCCNCCTGGC GACGCCCTGG 180
GGGGTTGGGA AGCCAAGGAA GAGGAATGAG GAGNCACGCG CNTACAGNTC TCTCGAATNC 240
TGANAAGATC TGAAGGGGGG AACATATTTG TATTAGNATN NAAGTATGCT CTTTATCAGA 300
TAGAAAATTC ACGAACGTGT GGNATAAAAA GGGAGTCTTA AAGAAATNTA AGATGTGCTG 360
GGACTACTTA GCCTCCAANA CACAGATNCC TGGATGGAGC T 401

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 459 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

AAAANNAAAA AAAATCTCCC AGGCCTAACA TAATTNTCAG GAAAGAAATT TCAGTAGTTG 60
NATCTCAGGG GAAATACAGG AAGTTAGCCT GGAGTAAAG TCAGTGTGTC CCTGCCCTT 120
TGCTANATTG CCCGTGCCTC ACAGTGCTCT CTGCCTGTGA CGACAGCTCC NCAGAAAGTTC 180
GGAGGATATA ATGGAATTCA TTGTGTACTG AAGAATGGAT AGAGAACTCA AGAAGGAAAT 240
TGGAAACTGG AAGCAAATGT AGGGGTAATT AGACACCTGG GGCTTCTGTG GGGGTCTGCT 300
TGGCGGTGAG GGGGCTCTAC ACAAGCTTCC TTTCCGTCAT GCCGNCCCCC ACCCTGGCTC 360
TGACCATTCT GTTCTCTCTG GCAGGTCATG ATGATGGGCA GCGCCCGAGG CGCGGAGCTG 420
CTGCTGCTCC ACGGCGCGGA GCCCACTGCT CCGACGCCG 459

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 390 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

①
AANAAAAAG AAATNGATAA NATAGAGGAA TGAACANATT AAAATCAAAA AACANAACAN 60
AGACATAATA AAAAACGAGA ATGTTCTAGA CNTAATCATA ATTATAAAGC TCAAGACTCA 120
TTGATATNAA GGADATTGAA GGGAAATCTT AACTAGCACA ANNGNATNAA AAAANAATTC 180
CCACGACACC GCCACTCTCA ACGCATCCGT GCTCGACACT GCCCGGGAGG TCNTCCTGGA 240
CACGCTGGTG GTNCTCCACC GGNCCGGGGC ACGTCTGGAC GTGCGCGATG CCTGGGNCCG 300
NCTACCCGTG GTACCTGACT GAGGACCTGG GCCATCCCGA TTTCGCNGGG TANCTCNGN 360
GGCTGNGGGG GCCAANAGAG GNCANTACCC 390

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 214 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

CCTGCNACGA CCCCGCCACT CTCACCCGAC CCGTGACGA CGCTGTCCGG GAGGGTTTCC 60
TGGACACGCT GGTGGTGCTG CACCGGGCCG GGGNGCGGTT GGACGTGCGC GATGCCTGGG 120
GCCGCCTNCC CGTGGNACCT GGTGAGGAG CTGGGNCATC GCGATGTCGC ACGGTACCTG 180
CGCGCGTTGC GGGGGGCACC AGAGGNNAGT NACC 214

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 235 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

NCTCTCACGG TGGGGAGGCC AACTGCGCCG AACCCGCCAC TCTCACCCGA CCCGCGCACG	60
ACGGTGCCCCG GGAGGGGTTC CTGGACACGC TGGTGGTGCT GCACCGGGCC GGGGCGCGGC	120
TGGACGTTTCG NGATGCCTGG GGGNTCTNTC CGTNGNACCT GGCTGAAGAG CTGCNNCATC	180
GNGATGTCGC ACGGCCNCTG TGTGNGGNTG CGGGGGGCAC CATAGGTCAG TNTCC	235

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 573 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

NAAGTATGAG CGAAACNAAT TGTGGTTTGA GAANAGGNAA TCGTAGGGAA CTTCGGGATC	60
CCNCNGGGAN CNCCAGAACC TGAGNCGCCN ATTGGAAATN ACAAACTGNC TGNATCACTC	120
CGNACCAGGT NCAAAAGATA CCTGGGGANG CGGGAAGGGA AAGACNACAT CNAGACCGCC	180
TTCGCNCCTN GGNATTGTGA GCAGCCTCTG AGACTCATTN ATATNACACT CTCGTNTTTC	240
TTCTTACAAC CCTGCGGNCC GCGCGGTCGC GCTTCTCTG CCCTCCGCCG GGTGGACCTG	300
GAGCGCTTGA GCGGTCGGCG CGCCTGGAGC AGCCAGGCGG NCAGTGGACT AGCTGCTGGA	360
CCAGGGAGGT GTGGGAGAGC GGTGGCGGCG GGTACATGCA CGTGAAGCCA TTGCGAGAAC	420
TTTATCCATA AGTATTTCAA TACCGGTAGG GACGGCAAGA GAGGAGGGCG GGATGTGCCA	480
CACATCTTTG ACCTCAGGT TCTAACGCCT GTTTCTTTC TGCCCTCTGC AGACAACCCC	540
CGATTGAAAG AACCAGAGAG GCTCTGAGAA ACC	573

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 434 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

CCCCATCGCG CCTTGGGANT GTGAGCNACC ATTGAGACTC ATNAATATAG CACTCGTTTT	60
TCTTCTTGCA ACCCTGCCCN CCGCGCGGTC GCGCTNTCTC TGCCCTCCGC NGGGTGGACC	120
TGGAGCGAGC GCTTGAGCGG TCGGTCGGCG CNCCTGGANC AGCCAGGCGG GCAGTGGACT	180
ACCTNCTGGA CCAGGGACCT GTGGGAGAGC GGTGNCGGCG GGTACATGCA CGTGAAGCCA	240
TTGCGAGAAC TTTATCCATA AGTATTTCAA TGCCGGTAGG GACGGCAAGA GAGGAGGGCG	300
GGATGTNCCA CACATCTTTG ACCTCAGGTT TCTAACGCCT GTTTTCTTTC TGCCCTCTGC	360
AGACATCCCC GATTGAAAGA ACCAGAGAGG CTCTGAGAAA CCTCCGAAA CTTAGNTCAT	420
CANTCGCCGN AAAA	434

(2) INFORMATION FOR SEQ ID NO:30:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 502 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

AGAAATTAGA TCATCAGTCA CCGATCCTCC TACAGGGNCA CAACTGNCCC CGCCACAACC	60
CACCCCGNTT TCGTAGTTTT CATTTAGAAA ATAGAGCTTT TAAAAATGTC CTGCCTTTTA	120
ACGTAGATAT ATGCCTTCCC CCACTACCGN AAATGTCCAT TTATATCATN TTTTATATAT	180
TCTTATAAAA ATGTAAAAAA GAAAAACACC GCTTCTGCCT TTTCAGTGTG TTGGAGTTTT	240
CTGGAGTGAG CACTCAGGCC CTAAGCGCAC ATTCATGTGG GCATTTCTTG CGAGCCTCGC	300
AGNCTCCGGA AGCTGTGAC CTCGAGGGGG GGNCCGGTAC CCAATTCGCC CTATAGTGAG	360
TCGTATTACA ATTCAGTGGN CGNCGNTTTT ACAACGTCGG TGGACTGGGA AAACCCCGGN	420
GTTACCCAAC TTTAATCGNC TTGGAGGACA TCCCCCTTTT CGCCAGNTGG GGTATAGNG	480
AAGAGGGCCN CACCNNTCGC CC	502

(2) INFORMATION FOR SEQ ID NO:31:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 503 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

91

CANCNATNTN	CGGCATTTCT	NGNGAGCCTC	GTAGTCTCCG	GATGNTGTCG	ACCTCGAGGG	60
GGGGNCCNGT	ACCCAATTCG	NCCTATNGTG	AGTCGTNTTA	CAATTCCTG	GCCGCCGTTT	120
TNACAACGTC	GNTGNACTGG	GAAAACCCTG	GTGTTACCCA	ACTTNAATGT	CCTTGNAGNA	180
CATCCCCCTT	TNCGCCAGCT	GGTGTAATAG	CGANGAGGCC	CGCACCGATC	GCCCTTCCCA	240
ACAGTTGNGC	AGCCTGAATG	GCGAATGGAA	ATTGTAAGCG	TTAATATTTT	GTAAAAATTC	300
GCGTTANATC	NTCGGTTAAN	TCAGCTCATN	TTTTATCCAA	TAGGCCGANA	TCGGCANAAT	360
CCCCAATAAA	TCAANAGAAT	AGACCGAGAT	AGGGTTGAGT	GTCGTTCCAG	TTNGGGAACA	420
NGAGTCCACT	ATTAAAGANC	GTAGNCTCNA	ACGTCANAGG	GCGAAAAACC	NTNTTTCAGN	480
GGATTGGNCC	ACTACGCNTA	NCC				503

(2) INFORMATION FOR SEQ ID NO:32:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 515 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

CANCNATNTN	CGGCATTTCT	NGNGAGCCTC	GTAGTCTCCG	GATGNTGTCG	ACCTCGAGGG	60
GGGGNCCNGT	ACCCAATTCG	NCCTATNGTG	AGTCGTNTTA	CAATTCCTG	GCCGCCGTTT	120
TNACAACGTC	GNTGNACTGG	GAAAACCCTG	GTGTTACCCA	ACTTNAATCG	CCTTGNAGNA	180
CATCCCCCTT	TNCGCCAGCT	GGTGTAATAG	CGANGAGGCC	CGCACCGATC	GCCCTTCCCA	240
ACAGTTGNGC	AGCCTGAATG	GCGAATGGAA	ATTGTAAGCG	TTAATATTTT	GTAAAAATTC	300
GCGTTANATC	NTCGGTTAAN	TCAGCTCATN	TTTTATCCAA	TAGGCCGANA	TCGGCANAAT	360
CCCCAATAAA	TCAANAGAAT	AGACCGAGAT	AGGGTTGAGT	GTCGTTCCAG	TTNGGGAACA	420

NGAGTCCACT ATTAAAGANC GTAGNCTCNA ACGTCANAGG GCGAAAAACC NTNTTTCAGN 480
GGATTGGNCC ACTACGCNTA NCCATCACCC TATTC 515

(2) INFORMATION FOR SEQ ID NO:33:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 89 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

Ile Gln Val Met Met Met Gly Ser Ala Arg Val Ala Glu Leu Leu Leu Leu
1 5 10 15
His Gly Ala Glu Pro Asn Cys Ala Asp Pro Ala Thr Leu Thr Arg Pro Val
20 25 30
His Asp Ala Ala Arg Glu Gly Phe Leu Asp Thr Leu Val Val Leu His Arg
35 40 45 50
Ala Gly Ala Arg Leu Asp Val Arg Asp Ala Trp Gly Arg Leu Pro Val Asp
55 60 65
Leu Ala Glu Glu Leu Gly His Arg Asp Val Ala Arg Tyr Leu Arg Ala Ala
70 75 80 85
Ala Gly Gly Thr

(2) INFORMATION FOR SEQ ID NO:34:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 88 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

Ile Gln Val Met Met Met Gly Ser Ala Arg Val Ala Glu Leu Leu Leu Leu

1 5 10 15
His Gly Ala Glu Pro Asn Cys Ala Asp Pro Ala Thr Leu Thr Arg Pro Val
20 25 30
His Asp Ala Ala Arg Glu Gly Phe Leu Asp Thr Leu Val Val Leu His Arg
35 40 45 50
Ala Gly Ala Arg Leu Asp Val Arg Asp Ala Trp Gly Arg Leu Pro Val Asp
55 60 65
Leu Ala Glu Glu Arg Gly His Arg Asp Val Ala Gly Tyr Leu Arg Thr Ala
70 75 80 85
Ala Gly Asp

D7
Cm